CLAIM LISTING

Following is a complete listing of the claims that replaces all prior versions and listings.

1 (previously presented). A method for identifying a subject at risk of melanoma, which comprises detecting the presence or absence of one or more polymorphic variations associated with melanoma in a nucleic acid sample from a human subject,

wherein the polymorphic variation is detected in an intron of a region between about the position of rs1267618 and about the position of rs1639679;

whereby the presence of the one or more polymorphic variations is indicative of the subject being at risk of melanoma.

2 (original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3 (previously presented). The method of claim 1, wherein the one or more polymorphic variations comprises a polymorphic variation at a site selected from the group consisting of rs1639679, rs1267646, rs1267636, rs1639675, rs1267649, rs1267609, rs1267625, rs1267601, rs1267606 and rs1267621.

4 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1639679 polymorphic variation.

5 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267636 polymorphic variation.

6 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1639675 polymorphic variation.

7 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267649 polymorphic variation.

8 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267609 polymorphic variation.

9 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267601 polymorphic variation.

10 (cancelled).

11 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises the haplotype CTTG corresponding to rs1639679, rs1267646, rs1267606 and rs1267621 positions.

12 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises the haplotype ATGA corresponding to the rs1639679, rs1267646, rs1267606 and rs1267621 positions.

13 (original). The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

14 (previously presented). The method of claim 13, wherein the oligonucleotide is selected from the group consisting of GTAATGTTGAAACTACAATTACCA (SEQ ID NO: 45);

GAAACAGGCTTCAATTCATCTT (SEQ ID NO: 46);
ACATAGAGGCAGGACTGTCA (SEQ ID NO: 47);
ATTAGGACATGGCTGAGATATTCA (SEQ ID NO: 48);
GGACTCTGCTTATTCTACCCA (SEQ ID NO: 49);
AGAGATTGTGCTTCCCAAATC (SEQ ID NO: 50);
GAATTAGTGAACTCTGGAAAGT (SEQ ID NO: 51);
GAAATATGTTTGGAAAATTGTTCT (SEQ ID NO: 52);
CTACAAAGCAAGACAGGACTAA (SEQ ID NO: 53);
CCAAGATAAGAATCTGTTTTACC (SEQ ID NO: 54);
AATGTTCTGAATTTTTCCAACTAA (SEQ ID NO: 55); and
TTATAATTTAGTGGGGAACAGAA (SEQ ID NO: 56).

15-48 (cancelled).

49 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267646 polymorphic variation.

50 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267625 polymorphic variation.

51 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267606 polymorphic variation.

52 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267621 polymorphic variation.

53 (previously presented). The method of claim 3, wherein the one or more polymorphic variations comprises a polymorphic variation at a site selected from the group consisting of rs1267649, rs1267609 and rs1267601.